

165712

From: Bowman, Amy
Sent: Wednesday, September 14, 2005 2:24 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/738,413

Hello,
I need SEQ ID NO: 1 in application 10/738,413 searched, length limited to 21 nucleotides.
Thank you,
Amy Bowman
AU 1635
mail REM 2C18
REM 2C31
571-272-0755

CRPS

EDWARD HART

9/19/05

9/19/05
-NA
P1

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* Example: 1610

➤ *Relevant prior art found, search results used as follows:*

- 102 rejection
- 103 rejection
- Cited as being of interest.
- Helped examiner better understand the invention.
- Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- Results verified the lack of relevant prior art (helped determine patentability)
- Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



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GenCore version 5.1.6

On nucleic - nucleic search, using sw model

Run on: September 17, 2005, 09:08:30 ; Search time 1540 Seconds
(without alignments)
660.753 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uaggaccggccaggugcucutt 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched:

Total number of hits satisfying chosen parameters: 892778

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Maximum Match 0%
Minimum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_bt:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_stb:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
c 1	13.2	62.9	19	4	DOGP20402	RESULT 1 DOGP20402/c LOCUS DOGP20402 19 bp DNA, linear DEFINITION Dog (Clone: CXX-204) primer for STS 204, 3', end. ACCESSION L15665 VERSION L15665.1 KEYWORDS PCR identification; PCR primer; STS. SEGMENT 2 of 2 SOURCE Canis familiaris (dog) ORGANISM Canis familiaris (dog) BIOLOGICAL_ASPECTS Mammalia; Metacara; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis. REFERENCE 1 (bases 1 to 19) AUTHORS Ostrander,E.A., Sprague,G.F.Jr. and Rine,J.D. TITLE Identification and characterization of dinucleotide repeat (CA)n MARKERS FOR GENETIC MAPPING IN DOG JOURNAL Genomics (1993) In Press COMMENT Original source text: Canis familiaris (library: E. Ostrander, in pBluescript+) adult spleen DNA. Submitted by: Human Genome Center, Lawrence Berkeley Laboratory, Berkeley, CA 94720, USA
c 2	12.8	61.0	20	6	AR125581	L15665 Dog (Clone: AR125581) Sequence PCR Buffer: PCR buffer (Perkin-Elmer/Cetus) PCR Profile: Denaturation: 94 degrees C for 1.00 minute Annealing: 55 or 59 degrees C for 0.45 minute Polymerization: 74 degrees C for 1.00 minutes PCR Cycles: 33 Final Extension: 74 degrees C for 5.00 minutes.
c 3	12.8	61.0	21	6	BD173609	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 4	12.8	61.0	21	6	BD173609	PCR Buffer: PCR buffer (Perkin-Elmer/Cetus) PCR Profile: Denaturation: 94 degrees C for 1.00 minute Annealing: 55 or 59 degrees C for 0.45 minute Polymerization: 74 degrees C for 1.00 minutes PCR Cycles: 33 Final Extension: 74 degrees C for 5.00 minutes.
c 5	12.4	59.0	19	12	AB059169	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 6	12.4	59.0	20	6	AR315617	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 7	12.4	59.0	20	6	AX4687667	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 8	12.2	58.1	20	6	AR257223	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 9	12.2	58.1	20	6	AX294943	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 10	12	57.1	17	6	AX264519	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 11	12	57.1	17	6	AX264520	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 12	12	57.1	17	6	AX264523	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 13	12	57.1	17	6	AX264524	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 14	12	57.1	17	6	AX687762	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 15	12	57.1	17	6	AX687763	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 16	12	57.1	17	6	AX687764	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 17	12	57.1	17	6	AX687765	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 18	12	57.1	17	6	AX687766	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov
c 19	12	57.1	17	6	AX687767	AR125581 Sequence BD173609 Method for AR125581 AR069159 Synthetic AR315617 Sequence AR42804 Sequence e-mail: Bostrandereb@lbl.gov

ALIGMENTS

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1. .19	/organism="Canis familiaris" /mol_type="genomic DNA" /db_xref="taxon:9615" /tissue_type="spleen" /dev_stage="adult" /tissue_lbb="E. Ostrander, in pBluescript+," /evidence=experimental			62.9%; Score 13.2; DB 4; Length 19;

QY	5 ACCUGCCAGAUGCUCUT 20 : : : : 5 ACCUGCCAGAUGCUCUT 20
Db	19 GACCTGCCACAGACUTT 2
RESULT 2	
AR125581	AR125581 Sequence 82 from patent US 6177273. 20 bp DNA linear PAT 16-MAY-2001
DEFINITION	
ACCESSION	AR125581
VERSION	AR125581.1 GI:14111643
KEYWORDS	Unknown.
SOURCE	ORGANISM
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 20) Bennett,C.Frank. and Cowser,L.M.
TITLE	Antisense modulation of integrin-linked kinase expression
JOURNAL	patent: US 6177273-A 82 23-JAN-2001;
FEATURES	Location/Qualifiers
source	1. .20 /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
RESULT 3	
BD171375	BD171375 Method for detecting bronchial asthma risk factor. 21 bp DNA linear PAT 18-FEB-2003
LOCUS	BD171375
DEFINITION	Method for detecting bronchial asthma risk factor.
ACCESSION	BD171375
VERSION	BD171375.1 GI:28412665
KEYWORDS	JP 2002218997-A/10.
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1 (bases 1 to 21)
AUTHORS	Nakamura,Y. and Tamari,M.
JOURNAL	Method for detecting bronchial asthma risk factor Patent: JP 2002218997-A/10 06-AUG-2002;
COMMENT	ONSUKE PHARMACEUTICAL CO LTD
OS	Artificial Sequence
PN	JP 2002218997-A/10
PD	06-AUG-2002
PP	05-JAN-2001 JP 2001017076
PI	YUSUKE NAKAMURA, MAYUMI TAMARI
PC	C12Q1/68, C12N15/09, C12N15/00
CC	Primer sequence (F5) for PCR
FH	Key
FT	source
FEATURES	1. .21 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
source	/organism='Artificial Sequence'.
ORIGIN	
RESULT 5	
AB069169	AB069169 Synthetic construct DNA, reverse primer for human STS sts-R-100A7R 19 bp DNA linear SYN 21-MAY-2003
LOCUS	AB069169
DEFINITION	Synthetic construct DNA, reverse primer for human STS sts-R-100A7R
ACCESSION	AB069169
VERSION	AB069169.1 GI:15129973
KEYWORDS	at 1336.
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1
AUTHORS	Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K., Mizushima,H., Arai,Y., Watanabe,N., Inazawa,J., Hosoda,F., Hori,A., Morohashi,A., Ohira,M., Nakagawa,A., Liu,S., Hoshi,M., Hori,A., Soeda,E.
JOURNAL	A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36 Genomics 74 (1), 55-70 (2001)
MEDLINE	21263192
PUBMED	11375902
REFERENCE	2 (bases 1 to 19)
AUTHORS	Hori,A.
TITLE	Direct Submission
JOURNAL	Submitted (04-AUG-2001) Akira Hori, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
FEATURES	Location/Qualifiers
source	1. .21 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
ORIGIN	
Query Match	Best Local Similarity 61.0%; Score 12.8; DB 6; Length 21;
Best Local Similarity	62.5%; Pred. No. 4.2e+04; Mismatches 10; Conservative 4; Indels 0; Gaps 0;

Miyagi 980-8575, Japan (E-mail:hori@email.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
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/organism="synthetic construct"
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1. -19
/note="reverse primer for human STS B10A7 at 1p36
B10A7R obtained from clones B10A7, Human BAC
library RPCI-11"

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Matches 12; Conservative 1; Pred. No. 7.1e+04; Mismatches 1; Indels 0; Gaps 0;
Qy 2 AGGACCTGCCAGAG 15
Db 3 AGGACCTGCCAGAG 16

RESULT 5
AR315617/c
LOCUS AR315617
DEFINITION Sequence 6154 from patent US 6559294.
ACCESSION AR315617
VERSION AR315617.1
KEYWORDS AR315617.1 GI:3170943
ORGANISM Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffels,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
TITLE Chlamydia pneumoniae poly nucleotides and uses thereof
FEATURES JOURNAL Patent: US 6559294-A 6154 06-MAY-2003;
Bsource Location/Qualifiers 1..20
/organism="unknown"
/mol_type="genomic DNA"

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Best Local Similarity 59.0%; Score 12.4; DB 6; Length 19;
Matches 12; Conservative 1; Pred. No. 7.1e+04; Mismatches 1; Indels 0; Gaps 0;
Qy 2 AGGACCTGCCAGAG 15
Db 3 AGGACCTGCCAGAG 16

RESULT 6
AR315617/c
LOCUS AR315617
DEFINITION Sequence 6154 from patent US 6559294.
ACCESSION AR315617
VERSION AR315617.1
KEYWORDS AR315617.1 GI:3170943
ORGANISM Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Popoff,I.
TITLE Antisense modulation of PTPN2 expression
JOURNAL Patent: US 6485974-A 78 26-NOV-2004;
FEATURES JOURNAL Location/Qualifiers 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match
Best Local Similarity 58.8%; Score 12.2; DB 6; Length 20;
Matches 10; Conservative 4; Pred. No. 9.3e+04; Mismatches 3; Indels 0; Gaps 0;
Qy 1 UAGGACCCAGUCU 17
Db 2 TAGTACTGACAGCT 4

RESULT 7
AX462804/c
LOCUS AX462804
DEFINITION Sequence 548 from Patent EP1217079.
ACCESSION AX462804
VERSION AX462804.1
KEYWORDS AX462804.1 GI:21886030
ORGANISM Agellops tauschii
Aegilops tauschii
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Aegilops.

REFERENCE 1
AUTHORS Bernard,M., Sourdille,P. and Guyomarch,H.
TITLE Microsatellite markers from *Triticum tauschii*
JOURNAL Patent: EP 1217079-A 548 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES Location/Qualifiers 1..20
/organism="Agellops tauschii"
/mol_type="unassigned DNA"

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Best Local Similarity 58.1%; Score 12.2; DB 6; Length 20;
Matches 11; Conservative 3; Pred. No. 9.3e+04; Mismatches 3; Indels 0; Gaps 0;
Qy 4 GACCCGCGGCGCTT 20
Db 4 GACCCGCGGCGCTT 20

RESULT 10	AX264519/C	AX264519	17 bp	DNA	linear	PAT 26-OCT-2001	KEYWORDS	Homo sapiens (human)
LOCUS		Sequence 1910	from Patent	WO0173002.			SOURCE	Homo sapiens (human)
DEFINITION							ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
VERSION		AX264519					REFERENCE	1. Kmiec, B.B., Gamper, H.B. and Rice, M.C.
KEYWORDS							AUTHORS	Kmiec, B.B., Gamper, H.B. and Rice, M.C.
SOURCE							TITLE	Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
ORGANISM							JOURNAL	Patent: WO 0173002-A 1914 04-OCT-2001;
REFERENCE							UNIVERSITY OR	UNIVERSITY OF DELAWARE (US)
AUTHORS							FEATURES	Location/Qualifiers
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RESULT 11							DEFINITION	Sequence 1915 from Patent WO0173002.
LOCUS		AX264520	17 bp	DNA	linear	PAT 26-OCT-2001	VERSION	17 bp
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ACCESSION		AX264520					SOURCE	
VERSION		AX264520.1	GI:16513319				ORGANISM	
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE								
AUTHORS								
TITLE								
JOURNAL								
FEATURES								
ORIGIN								
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DEFINITION							VERSION	17 bp
ACCESSION							KEYWORDS	
VERSION							SOURCE	
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SOURCE							REFERENCE	
ORGANISM							AUTHORS	
REFERENCE							TITLE	
AUTHORS							JOURNAL	
TITLE							FEATURES	
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Matches		91.7%	Pred.	No.	1.2e+05;			
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TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281759-A 494 05-FEB-2003;
Aeconica, Inc. (US)
FEATURES Location/Qualifiers
Source
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 /mol_type="unassigned DNA"
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ORIGIN

Query Match 57.1%; Score 12; DB 6; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 10 CCGUGCCUCUTT 21
 ||||:||:||:
Db 17 CCAGTGCTCTTT 6

RESULT 15

AX687763/c
LOCUS AX687763
DEFINITION Sequence 495 from Patent EP1281759.
ACCESSION AX687763
VERSION AX687763.1
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
 mdz12

JOURNAL Patent: EP 1281759-A 495 05-FEB-2003;
Aeconica, Inc. (US)

FEATURES Location/Qualifiers
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 1. .17
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ORIGIN

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Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 10 CCAGUGCCUCUTT 21
 ||||:||:||:
Db 16 CCAGTGCTCTTT 5

Search completed: September 17, 2005, 10:47:56
 Job time : 1546 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 09:06:56 ; Search time 256 seconds
(without alignments)
485.604 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uaggaccugccagugcucutt 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2380332

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_GeneSeq_15Dec04:*

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2: geneSeqn1990s;*

3: geneSeqn2000s;*

4: geneSeqn2001as;*

5: geneSeqn2001bs;*

6: geneSeqn2002as;*

7: geneSeqn2002bs;*

8: geneSeqn2003as;*

9: geneSeqn2003bs;**

10: geneSeqn2003cb;**

11: geneSeqn2003db;**

12: geneSeqn2004as;*

13: geneSeqn2004bs;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
C 1	15	71.4	20	4	AA16582	Aa16582 Oculocutaneous albinism 1B causative gene related PCR primer #2.
C 2	13.6	64.8	20	12	ADP6070	Adp6070 Human Jag
3	13.6	64.8	20	12	ADP8033	Adp8033 Human Jag
4	13.2	62.9	20	12	ADH6423	Adh6423 Human glu
5	13.2	62.9	20	12	ADH64554	Adh64554 Human glu
6	13.2	62.9	20	12	ADH31908	Adh31908 Human glu
7	12.8	61.0	17	11	ADL48810	Adl48810 Human ICK
8	12.8	61.0	17	11	ADL48391	Adl48391 Human ICK
9	12.8	61.0	19	12	ADL4399	Adl4399 PCR prime
10	12.8	61.0	20	4	AAF69353	Aaf69353 Integrin
c 11	12.8	61.0	20	10	ADB43705	Adb43705 Human RNS
c 12	12.8	61.0	20	10	ADL525330	Adl525330 Intestina
c 13	12.8	61.0	20	12	ADH4183	Adh4183 Human neu
c 14	12.8	61.0	20	12	ADH4371	Adh4371 Human glu
c 15	12.8	61.0	20	12	ADH3823	Adh3823 Human glu
c 16	12.8	61.0	20	12	ADH8065	Adh8065 Primer of
c 17	12.8	61.0	20	12	ADJ58890	Adj58890 Human int
c 18	12.8	61.0	20	12	ADM4533	Adm4533 Human mPG
c 19	12.8	61.0	20	12	ADM15285	Adm15285 Human mPG
c 20	12.8	61.0	20	12	ADM15022	Adm15022 Human mPG

ALIGNMENTS

Query Match 71.4%; Score 15; DB 4; Length 20

CG the human glucocorticoid receptor gene. NOTE: The present sequence contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 CC
 XX
 SQ Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;
 Query Match Best local similarity 61.1%; Pred. No. 1.3e+04; 3; Mismatches 11;保守性 4; Length 20;
 Matches 11;保守性 4; Length 20;
 Qy 4 GACCUGCCAGCTGCTT 21
 Db 1 GTCCTTCACGCTCTT 18

RESULT 7
 ADL48810
 ID ADL48810 standard; RNA; 17 BP.
 XX
 AC ADL48810;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human IKK-gamma substrate sequence #1320.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PGDR; IkappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;
 KW substrate; ds.
 XX
 OS Unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002W0-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PT Blatt L, Chowrira B, Haeberli P, McSwiggen J, Fosnaugh K;
 XX
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 2343; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a

CC target RNA in a cell. The present RNA sequence represents a human IKK-gamma substrate sequence.
 CC
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 8 G; 0 T; 2 U; 0 Other;
 Query Match Best local similarity 87.5%; Pred. No. 2e+04; 0; Mismatches 14;保守性 0; Length 17;
 Matches 14;保守性 0; Length 17;
 Qy 1 UAGGACUCGCAUGC 16
 Db 2 UAGGACUCGCAUGC 17

RESULT 8
 ADL48391
 ID ADL48391 standard; RNA; 17 BP.
 XX
 AC ADL48391;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human IKK-gamma substrate sequence #901.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PGDR; IkappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;
 KW substrate; ds.
 XX
 OS Unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002W0-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PT Blatt L, Chowrira B, Haeberli P, McSwiggen J, Fosnaugh K;
 XX
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 1924; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a

CC	target RNA in a cell. The present RNA sequence represents a human IKK-	RESULT 10
CC	gamma substrate sequence.	AARF9353
XX	Sequence 17 BP; 3 A; 5 C; 7 G; 0 T; 2 U; 0 Other;	ID AARF9353
SQ	Best Local Similarity 61.0%; Score 12.8; DB 11; Length 17;	XX
	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	AC AARF9353;
QY	1 UAGGCCUGCGAGUGC 16	XX
	: : :	DT 18-APR-2001 (first entry)
DB	1 UAGGCCUGCGAGUGC 16	XX
	: : :	DE Integrin-linked kinase 3'UTR targeted oligonucleotide #2.
SQ	RESULT 9	KW Antisense; integrin-linked kinase; hik; infection; tumour; inflammation;
ADL14399	ADL14399 standard; DNA; 19 BP.	KW BB.
ID	ADL14399;	XX
AC	XX	OS Homo sapiens.
XX	XX	XX
AC	ADL14399;	PN US6177273-B1.
XX	XX	XX
DT	20-MAY-2004 (first entry)	PD 23-JAN-2001.
XX		XX
DE	PCR primer used to amplify the UGT Y486D isoform SeqID 8.	PF 26-OCT-1999; 99US-00428219.
XX		XX
KW	drug metabolic ability; UGT; UDP- glucuronosyl transferase;	XX
KW	gene analysis; liver function; Crigler-Najjar syndrome type I;	PA (ISIS-) ISIS PHARM INC.
KW	Crigler-Najjar syndrome type II; Gilbert syndrome;	XX
KW	Dubin-Johnson syndrome; Rotor syndrome; PCR; primer; BB.	PI Bennett CF, Cowart LM;
OS	Synthetic.	XX
XX		DR WPI: 2001-137069/14.
PN	WO2004016814-A1.	XX
XX		PT Novel antisense compounds capable of modulating expression of human
PD		PT Integrin-linked kinase, useful for diagnosis, prophylaxis and treatment
XX		PT of diseases, e.g. tumors, associated with expression of the kinase.
PP	13-FEB-2003; 2003WO-JP001475.	XX
XX		PS Claim 3; Col 45; 40pp; English.
PR	12-AUG-2002; 2002JP-00235029.	XX
XX		CC The present invention relates to an antisense compound 8 to 30 bases in
PA	(UNI-) UNIV JAPAN SEC SHIGA MBD.	CC length targeted to the 5' untranslated (5'UTR) region, the coding region or
XX		CC the 3' UTR region human Integrin-linked kinase (hik). The antisense
PI	Sato H, Fujiyama Y, Yamamoto K;	CC oligonucleotides are useful for inhibiting the expression of human hik in
XX		CC human cells or tissues, in vitro. The oligonucleotides can be utilized
PI		CC for diagnostics, therapeutics for the treatment of diseases associated
XX		CC with the expression of hik, prophylaxis e.g. to prevent or delay
DR	WPI; 2004-203813/19.	CC infection, inflammation or tumor formation and as research reagent
XX		XX
PT	Estimation of drug metabolic activity by analyzing mutations in	SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
PT	glucuronosyltransferase gene, useful in studying drug metabolism, gene	Query Match, 61.0%; Score 12.8; DB 4; Length 20;
PT	analysis and clinical examination e.g. of diseases.	Best Local Similarity 68.8%; Pred. No. 2e+04; Mismatches 11; Conservative 3; Indels 0; Gaps 0;
PS	Disclosure; SEQ ID NO 8; 33pp; Japanese.	DB 3 AGAACCTTCAGCTCT 18
XX		QY 2 AGAACCTTCAGCTCT 18
CC	This invention relates to a novel method for examining the drug metabolic	DB 3 AGAACCTTCAGCTCT 18
CC	ability of UGT (uridine-glucuronosyl transferase). Specifically, it refers	QY 2 AGAACCTTCAGCTCT 18
CC	to the use of nucleic acid chips and/or arrays with an appropriate	DB 3 AGAACCTTCAGCTCT 18
CC	oligonucleotide probe to detect mutations existing in exon 5 of the UGT	QY 2 AGAACCTTCAGCTCT 18
CC	gene. The present invention describes the method as useful for studying	DB 3 AGAACCTTCAGCTCT 18
CC	diseases that are associated with abnormal liver function including	QY 2 AGAACCTTCAGCTCT 18
CC	drug metabolism, gene analysis and for the clinical examination of	DB 3 AGAACCTTCAGCTCT 18
CC	Crigler-Najjar syndrome types I and II, Gilbert syndrome, Dubin-Johnson	QY 2 AGAACCTTCAGCTCT 18
CC	syndrome and Rotor syndrome. This oligonucleotide sequence is a PCR	DB 3 AGAACCTTCAGCTCT 18
CC	primer used to amplify a UGT DNA isoform, given in an exemplification of	QY 2 AGAACCTTCAGCTCT 18
CC	the invention.	DB 3 AGAACCTTCAGCTCT 18
SQ	Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 U; 0 Other;	QY 2 AGAACCTTCAGCTCT 18
	Best Local Similarity 61.0%; Score 12.8; DB 12; Length 19;	DB 3 AGAACCTTCAGCTCT 18
	Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	DB 3 AGAACCTTCAGCTCT 18
QY	3 GGACCCUGCCAGUGC 18	DB 4 GGACCTGGCTGTGTC 19
	: : :	
DB		
PN	WO20030554143-A2.	

XX
PD 03-JUL-2003.
XX
PR 25-OCT-2002; 2002WO-US034679.
XX
PR 25-OCT-2001; 2001US-0339525P.
PR 08-NOV-2001; 2001US-033929P.
PR 08-NOV-2001; 2001US-0338010P.
PR 09-NOV-2001; 2001US-0339363P.
PR 04-DEC-2001; 2001US-0337052P.
PR 28-MAR-2002; 2002US-0368919P.
XX
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Becker KD, Velicelebi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
XX
DR WPI; 2003-559131/52.
XX
PT Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic PT regions.
XX
PS Example 3; Page 291; 848pp; English.
XX
CC The present invention relates to a method (M1) for determining a predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or absence of an allelic variant of one or more polymorphic regions of one or more genes selected from uPA (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-degrading enzyme), KNL1 (Kinesin-like protein 1), LIPA (lysosomal acid lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the presence of at least one of the allelic variant of one or more polymorphic regions is indicative of a predisposition for or the occurrence of neurodegenerative disease. The genes are all located on chromosome 10. M1 is useful for determining a predisposition for or the occurrence of, and for treating neurodegenerative disease, particularly Alzheimer's disease. The present sequence is a PCR primer, which was used in the method of the invention.
XX
SQ Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 10; Length 20;
Best Local Similarity 68.8%; Pred. No. 2e+04; ID 2e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC
Qy 1 UGGGACCCUGCCAGUGC 16
Db 16 TAGGCTCTGCCATAGC 1
XX
RESULT 12
AD125330
ID AD125330 standard; DNA; 20 BP.
XX
AC ADH54183;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human neurodegenerative disease-related sequencing primer SeqID310.
XX
KW human; neurodegenerative disease; urokinase plasminogen activator; uPA; gamma-synuclein; SNCG; insulin degrading enzyme; IDE; kinesin-like protein 1; KNL1; lysosomal acid lipase; LIPA; tumour necrosis factor receptor SF6; TNFRSF6; Alzheimer's disease; PCR; primer; ss; sequencing.
XX
OS Homo sapiens.
XX
PN US2003224380-A1.
XX
PR 25-OCT-2002; 2002US-00282174.
XX
PD 04-DEC-2003.
XX
PR 25-OCT-2001; 2001US-0339525P.
PR 25-OCT-2001; 2001US-0338010P.
PR 03-NOV-2001; 2001US-0339363P.
PR 08-NOV-2001; 2001US-033629P.
PR 08-NOV-2001; 2001US-0338010P.

PR 09-NOV-2001; 2001US-0338363P.
 PT
 PR 04-DEC-2001; 2001US-0337052P.
 PR 28-MAR-2002; 2002US-0368919P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Becker KD, Velicelebi G, Elliott KJ, Wang X, Tanzi RE;
 PI Berttram L, Saunders AJ, Mullin KM, Sampson AJ;
 XX
 DR WPI; 2004-060538/06.
 XX
 PT Determining a predisposition for or the occurrence of neurodegenerative
 PT disease, particularly Alzheimer's disease, comprises determining the
 PT presence of a polymorphism in the uPA, SNGC, IDE, KNSL, LIPA or TNFRSF6
 PT gene.
 XX
 PS Example 3 ; SEQ ID NO 310; 205pp; English.
 XX
 CC This invention relates to a novel method of determining a predisposition
 for or the occurrence of neurodegenerative disease comprising detecting
 in a target nucleic acid obtained from the subject the presence of an
 allelic variant of polymorphic regions of human genes selected from
 CC urokinase plasminogen activator (uPA), gamma-synuclein (SNGC), insulin
 CC lipase (LIPA) and tumour necrosis factor receptor SF6 (TNFRSF6). The
 CC method is useful in determining the presence or predisposition to a
 CC neurodegenerative disease, particularly Alzheimer's disease. The present
 CC sequence is that of a sequencing primer which was used for sequencing of
 CC a region of the human KNSL gene in the exemplification of the invention.
 XX
 Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 61.0%; Score 12.8; DB 12; Length 20;
 Best Local Similarity 68.8%; Pred. No. 2e+04;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 CC
 Qy 1 UAGGACCUGCCAGUGC 16
 Qy 16 TAGGTCTGCCATTG 1
 Db
 XX
 RESULT 14
 ADH64371
 ID ADH64371 standard; DNA; 20 BP.
 AC
 XX
 AC ADH63823
 ID ADH63823 standard; DNA; 20 BP.
 AC
 XX
 AC ADH63823;
 ID ADH63823
 AC
 XX
 DT 25-MAR-2004 (first entry)
 DE Human glucocorticoid receptor-specific antisense oligonucleotide #6557.
 XX
 KW antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX
 OS Homo sapiens.
 XX
 PN WO2003099215-A2.
 XX
 PD 04-DEC-2003.
 XX
 PP 20-MAY-2003; 2003WO-US016084.
 PR 20-MAY-2002; 2002US-0381857P.
 PA (PHAA) PHARMACIA CORP.
 PI Crosby SD, Nalseth AE;
 PI XX
 DR WPI; 2004-035034/03.
 OS
 XX
 PN WO2003099215-A2.
 XX
 PD 04-DEC-2003.
 XX
 PR 20-MAY-2003; 2003WO-US016084.
 XX
 PR 20-MAY-2002; 2002US-0381857P.
 PA (PHAA) PHARMACIA CORP.
 PA XX
 PA Crosby SD, Nalseth AE;
 XX
 DR WPI; 2004-035034/03.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
 XX
 PS Claim 4 ; SEQ ID NO 657; 98pp; English.
 XX
 CC The invention comprises an antisense oligonucleotides that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX

SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 12; Length 20;
Best Local Similarity 62.5%; Pred. No. 2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0;
Gaps 0;
QY 6 CCUGCCAGUGCUU^{TT} 21
||: ||| :||:||:||:
Db 2 CCTTCCACTGCT^{TT} 17

Search completed: September 17, 2005, 10:22:12
Job time : 266 secs

GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model

Run on: September 17, 2005, 09:50:06 ; Search time 1907 Seconds
(without alignments)
419.166 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uaggaccugccagugucutt 21

Scoring table: IDENTITY_NUC

Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 15386

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST,*

1: gb_est1:
2: gb_est2:
3: gb_hrc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_g8s1:
9: gb_g8s2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

RESULT 1					
AZ496283	AZ496283	IM0332D09	AZ496283	20 bp	DNA linear GSS 05-OCT-2000
LOCUS	LOCUS	IM0332D09	DEFINITION	clone UUGCIM0332D09, genomic survey sequence.	
ACCESSION	ACCESSION	IM0332D09	VERSION	AZ496283.1	GI:10672347
KEYWORDS	KEYWORDS		GSS.		
SOURCE	SOURCE		ORGANISM	Mus musculus (house mouse)	
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	REFERENCE			1 (bases 1 to 20)	
AUTHORS	AUTHORS			Dunn, D., Royagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederauer, A., and Wright, D., Weiss, R.	
TITLE	TITLE			Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	JOURNAL			Unpublished (2000)	
COMMENT	COMMENT			Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177 Email: dclunn@genetics.utah.edu	
				Insert Length: 10000 Std Error: 0.00	
				Plate: 0332 row: D column: 09	
				Seq primer: CACACAGGAAACAGCTATGCC	
				Class: Plasmid ends	
				High quality sequence stop: 20.	
FEATURES	FEATURES		location/Qualifiers	1. .20	
Source	Source			/organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCIM0332D09" /sex="Male" /lab_host="E. Coli strain X110-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: pMD42IV; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnarefs/). The DNA	

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match Best Local Similarity 59.0%; Score 12.4; DB 8; Length 20; Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0; Qy 7 CUGCCAGAGCUCU 20 Db 1 CAGGCCGCTGCTT 14

RESULT 2

AZ42658/c
DEFINITION A2482658 IM0307116R Mouse 10kb plasmid UGCGC1 DNA library, Mus musculus genomic clone UGCGC1M0307116 R, genomic survey sequence.

ACCESSION A2482658
VERSION A2482658.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenem, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0307 row: L column: 16
Seq primer: CACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
Source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGC1M0307116"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGC1 library"
/note="Vector: pMD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnare/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match Best Local Similarity 54.3%; Score 11.4; DB 8; Length 19; Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Qy 5 ACCUGCCAGAGU 17 Db 13 ACCUGCCAGAGT 1

RESULT 3

AZ398062/c
DEFINITION A2398062 IM0163M14P Mouse 10kb plasmid UGCGC1 DNA library, Mus musculus genomic clone UGCGC1M0163M14 P, genomic survey sequence.

ACCESSION A2398062
VERSION A2398062.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenem, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0103 row: M column: 14
Seq primer: CGTTGTAAGAACGAGGGCACT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGC1M0163M14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGC1 library"
/note="Vector: pMD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnare/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of pBlasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL1-Gold (Stratagene) cells and selected for ampicillin resistance. "

ORIGIN

Query Match 48.6%; Score 10.2; DB 8; Length 20;
Best Local Similarity 60.0%; Pred. No. 3.4e+06;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGACCUCCAGGCCU 17
Db 19 GGCCTCGCTGCT 5

RESULT 4
CF337542
LOCUS CF337542 20 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--08-A10_b1 ATUMT-overexpressing transgenic rice plasmid cDNA clone
ACCESION JMT--08-A10, mRNA sequence.
VERSION CF337542.1
KEYWORDS EST
SOURCE
ORGANISM Oryza sativa (Japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr.

FEATURES
Source

1. -20
/organism="Oryza sativa (Japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nakdong"
/db_xref="taxon:39447"
/clone="JMT--08-A10"
/tr_sequ_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="AJM7-overexpressing transgenic rice plasmid cDNA Library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from *Arabidopsis* Jasmonic acid Carboxyl methyltransferase overexpression line."

FEATURES
Source

1. -20
/organism="Oryza sativa (Japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nakdong"
/db_xref="taxon:39447"
/clone="JMT--08-A10"
/tr_sequ_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="AJM7-overexpressing transgenic rice plasmid cDNA Library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from *Arabidopsis* Jasmonic acid Carboxyl methyltransferase overexpression line."

ORIGIN

Query Match 47.6%; Score 10; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.2e-06;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Query Match 46.7%; Score 9.8; DB 8; Length 19;
Best Local Similarity 53.8%; Pred. No. 5.2e+06;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

RESULT 5
AZ848554
LOCUS AZ848554 19 bp DNA linear GSS 21-FEB-2001
DEFINITION clone JUGC2M0149A07 R, genomic survey sequence.
ACCESSION AZ848554
VERSION AZ848554.1 GI:13031758
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bates 1 to 19)
REFERENCE Dunn,D., Avogari,A., Barber,M., Beacons,T., Duval,B., Hasil,C., Iseli,H., Longacre,S., Mahmoud,M., Meinen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000
Plate: 0149 row: A column: 07
Seq primer: CACAGGGAAACGCTATGACC
Class: Plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. -19
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/mol_type="genomic DNA"
/strain="C57BL/6J"
(db_xref="taxon:10090"
/clone="JUGC2M0149A07"
/sex="Male"
'/lab_host="E. Coli strain XL10-Gold, T1-resistant, F"
'/clone="Mouse 10kb plasmid JUGC1M library"
/note="Vector: pMD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares1/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of pBlasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL1-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Qy 7 CUGCCAGUGCUU 19
 Db 3 CTGCTAGTGCGT 15

Qy 7 CUGCCAGUGCUU 19
 Db 15 CTGCTAGTGCGT 3

RESULT 6
 AZ868070/C
 Locus AZ868070 19 bp DNA linear GSS 21-FEB-2001
 Definition 2M0179107F Mouse 10kb plasmid UGCGC library Mus musculus genomic
 Accession AZ868070
 Version AZ868070.1 GI:1371017
 Keywords GSS
 Source Mus musculus (house mouse)
 Organism Mus musculus

RESULT 7
 AI042533/c
 Locus AI042533 18 bp mRNA linear EST 30-JUN-1998
 Definition 010603.x1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA
 Accession AI042533
 Version AI042533
 Transformation-Related Protein 1, mRNA sequence.
 Keywords EST
 Source Homo sapiens (human)
 Organism Homo sapiens

JOURNAL
 REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Maenel, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niedernhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: daunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0179 row: I column: 07
 Seq primer: CGTTGAAACGACGGCCAGT
 Class: Plasmid ends
 High quality sequence stop: 19.
 FEATURES
 Source
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGC20179107"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, *Ti*-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGC library"
 /note="Vector: pM42nv, purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.Jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adopted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (gi|473214|gb|AF129072.1), a copy-number
 indicible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adopted mouse DNA was annealed to
 adopted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 46.7%; Score 9.8; DB 1; Length 19;
 Best Local Similarity 53.8%; Pred. No. 5.2e+06;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Query Match 7 CUGCCAGUGCUU 19
 Best Local Similarity 56.2%; Pred. No. 6.5e+06; Length 18;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 CUGCCAGUGCUU 21.
 Db 17 CCTTCAGGTCATT 2

RESULT 8
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 Locus AZ856028 21 bp DNA linear GSS 14-DEC-2000
 Definition 1M0531017F Mouse 10kb plasmid UGCGC library Mus musculus genomic
 Accession AZ856028
 Version AZ856028.1 GI:11793174
 Keywords GSS
 Source Mus musculus (house mouse)
 Organism Mus musculus

REFERENCE	Caryophyllales; Magnoliophyta; eudicotyledons; core eudicots;	
1	(bakes 1 to 11)	
AUTHORS	Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Sahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radefot,U.	
TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes	
JOURNAL	Plant J. 32 (5), 845-857 (2002)	
PMID	12262188	
PUBMED	12242658	
COMMENT	Contact: Weisshaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062051 Email: weisshaar@mpiz-koeln.mpg.de Insert Length: 11 Std Error: 0.00 Plate: 28 row: J column: 16 Seq primer: SP6: CATAGGATTAAGGTGACACTATAG.	
FEATURES	Location/Qualifiers	
Source	1. .11	
ORIGIN	<p>/organism="Beta vulgaris" /molecule="mRNA" /cultivar="KN2320 (double haploid, monogerml breeding line)" /line" /clone lib="MPIZ-ADIS-024-developing root" /note="Vector: pCMVSPORT6; Site1: Salt; Site 2: NotI; /db xref="taxon:101934" /clone="024-028-JT6" /clone_type="developing root" /lab_host="EMD1103" /clone lib="MPIZ-ADIS-024-developing root" /note="Vector: pCMVSPORT6; Site1: Salt; Site 2: NotI; /cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Eibbeck, Germany; contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: S96-SalI-CCAGCGCGTCG-5prime-cDNA-POLYA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project. Local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"</p>	
RESULT 10	Query Match 44.8%; Score 9.4; DB 5; Length 11; Best Local Similarity 72.7%; Pred. No. 7.6e-06; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
LOCUS	AZ772446 19 bp DNA linear GSS 16-FEB-2001	
DEFINITION	1M053016F Mouse 10kb plasmid tUGGCM library Mus musculus genomic clone UGGCM1M053016 F, genomic survey sequence.	
ACCESSION	AZ772446	
VERSION	AZ772446.1 GI:12895762	
KEYWORDS	GSS	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	1 (bases 1 to 19)	
AUTHORS	Dunn,D., Royagi,A., Barber,M., Beacon,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenem,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederauern,A., and Wright,D.,Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
TYPE	transcribed (cont)	

COMMENT	COMMENT
<p>Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5506 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0583 row: O column: 16 Seq primer: CGTGTGAAACGACGGCCAGT Class: plasmid ends</p>	<p>Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5506 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0465 row: C column: 08 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends</p>
<p>FEATURES Source</p> <p>High quality sequence stop: 19. Location/Qualifiers</p> <p>1. .19</p>	<p>FEATURES Source</p> <p>High quality sequence stop: 20. Location/Qualifiers</p> <p>1. .20</p>
<p>/organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCIM0583016" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource</p> <p>(http://www.Jax.org/resources/documents/dnarecs/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PW42 (gi 4721149b AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."</p>	<p>/organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCIM0465C08" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource</p> <p>(http://www.Jax.org/resources/documents/dnarecs/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PW42 (gi 4721149b AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."</p>
<p>ORIGIN</p> <p>Query Match: Best Local Similarity 44.8%; Score 9.4; DB 8; Length 19; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;</p> <p>Qy 5 ACTGCGCAGG 15 Db 6 ACTCTGACAGTG 16</p>	<p>ORIGIN</p> <p>Query Match: Best Local Similarity 44.8%; Score 9.4; DB 8; Length 20; Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;</p> <p>Qy 1 UAGGACGCCAGGCTCT 19 Db 19 TAGAACCTGAGGNGCGCT 1</p>
<p>RESULT 11</p> <p>A2625776/C</p> <p>LOCUS 20 bp DNA linear GSS 13-DEC-2000 DEFINITION clone UUGCIM0465C08 R, genomic survey sequence.</p> <p>ACCESSION A2625776 VERSION A2625776.1 GI:11747966</p> <p>KEYWORDS GSS.</p> <p>SOURCE Mus musculus (house mouse)</p> <p>ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.</p> <p>REFERENCE 1 (bases 1 to 20)</p> <p>AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederauer, A., and Wright, D. Weiss, R.</p> <p>TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts</p> <p>JOURNAL Unpublished (2000)</p>	<p>RESULT 12</p> <p>C1657853</p> <p>LOCUS CL657853</p> <p>DEFINITION PR1012c H07 - PR1012c.B21 (16) Mixed stage fomidae library of P. pacificus var. California Pristionchus pacificus genomic, genomic Survey sequence.</p> <p>ACCESSION C1657853</p> <p>VERSION C1657853.1 GI:50139888</p> <p>KEYWORDS GSS.</p> <p>SOURCE Pristionchus pacificus</p> <p>ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Diplopoda; Rhabditida; Pristionchus pacificus</p> <p>REFERENCE 1 (bases 1 to 16)</p> <p>AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Giesler, R. and Sommer, R.J.</p> <p>TITLE AppDB: an AceDB database for the nematode satellite organism Pristionchus pacificus</p> <p>JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)</p> <p>COMMENT Contact: Sommer, R.J.</p> <p>COMMENT Evolutionary Biology</p>

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel.: 0049 7071 601371
Fax: 0049 7071 601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.

osmid ends.
Location/Qualifiers
1. 16
/organism="Pristionchus pacificus"
/mol_type="Genomic DNA"
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/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of *P. pacificus*
var. California"
note="vector: pPifos-5 Fosmid vector"

ORIGIN

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Query Match 43.8%; Score 9.2; DB 9; Length 16;
Best Local Similarity 50.0%; Pred. No. 1e-07;
Matches 7; Conservative 4; Mismatches 3; Indels 0;
Qy : |||: :||: 8 UGCCAGGUCUUT 21
Db 3 TACAGCTACTCT 16

```

LOCUS A2027759/c
DEFINITION 20 kb DNA linear GSS 20-FEB-2001
VERSION A2027759
ACCESSION A2027759
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Islam,H., Longacre,S., Mahmud,M., Meinen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah, 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddumogene@utah.edu
 Insert length: 10000 Std error: 0.00
 Plate: 0104 row: E column: 22
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: Plasmid ends
FEATURES
Source
 1. 20
 Location/Qualifier
 High quality sequence stop: 20.
Source
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 /strain="C57BL/6J"
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 /clone="UGGC2M0104E22"
 /sex="Male"
 /lab_hb="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lb="Mouse 10kb Plasmid UGGC1M library"
 /note="Vector: PWD2nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnarefs/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214[gb] | B129721), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapter mouse DNA was annealed to adapter vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance. "

Query	Match	Score	Length	DB	DB
Matches	43.8%;	9.2;	20;	8;	8;
Best Local Similarity	57.1%;	Pred. No.	1e+07;	1e+07;	1e+07;
Matches	8;	Conservative	3;	Mismatches	3;
QY	8	UGCCAGUGCUCU	21	Indels	0;
Db	20	: : :	21	Gaps	0;
		TGCCAATGGAATG	7		

AJ591869/c	AU591869	20	bP	DNA	linear	GSS	15-JAN-2004
LOCUS	Arabidopsis thaliana	T-DNA	flanking sequence, left border, clone				
DEFINITION	594C10, genomic survey sequence.						
ACCESSION	AU591869						
VERSION	AU591869_1						
KEYWORDS	GSS; left border; T-DNA flanking sequence.						
SOURCE	Arabidopsis thaliana (thale cress)						
ORGANISM	Arabidopsis thaliana						
REFERENCE							
AUTHORS	Brunaud, V., Balzergue,S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Craud, C., De Rose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.						
TITLE	T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites						
JOURNAL	EMBO Rep. 3 (12), 1152-1157 (2002)						
MEDLINE	22363535						
PUBMED	12446565						
REFERENCE	2						
AUTHORS	Balzergue,S.						
JOURNAL	Direct Submission						
COMMENT	Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Crémieux, 91057 EVRY cedex, FRANCE						
PCR	PCR was performed on DNA from transformants of <i>Arabidopsis thaliana</i> plants from INRA (Versailles). The DNA fragment (16) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.verailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program Genoplante (http://www.genoplante.com and http://genoplante.info.intobioigen.fr).						
FEATURES	Location/Qualifiers						
source	1. .20 /organism="arabidopsis thaliana" /mol_type="genomic DNA" /cultivar="Wassilewskija" /db_xref="taxon:3702"						

/clone="594C10"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 1. .20
 /note="T-DNA flanking sequence
 left border"

ORIGIN

Query Match 43.8%; Score 9.2; DB 9; Length 20;
 Best Local Similarity 71.4%; Pred. No. 1e+07; Matches 10;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 ACCUGCCAGTCUC 18
 Db 17 ACTAGCCAGTCAC 4

RESULT 15

LOCUS A2661719 21 bp DNA linear GSS 14-DEC-2000
 DEFINITION Mouse 10kb plasmid UGCGCIM0540M24 F, genomic survey sequence.
 ACCESSION A2661719
 VERSION A2661719.1 GI:11798865
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

I. (bases 1 to 21)
 Dunn, D., Avagci, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D. Weiss, R.

Title Mouse whole genome scaffolding with paired end reads from 10kb

plasmid insert^B

Unpublished (2000)

Comment Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0540 row: M column: 24

Seq primer: CGTGTAAACGACGCCGAGT

Class: plasmid ends

high quality sequence stop: 21.

Location/Qualifiers

Source

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* X10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 43.8%; Score 9.2; DB 8; Length 21;
 Best Local Similarity 64.3%; Pred. No. 1e+07; Matches 9;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 AGGACUGSCAGUG 15
 Db 5 AGGACGTGAACTG 18

Search completed: September 17, 2005, 11:19:51
 Job time : 1914 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: September 17, 2005, 07:33:35 ; Search time 94 Seconds
Perfect score: 21 US-10-738-413-1
Sequence: 1 usggaccugccagucutt 21
Scoring table: IDENTITY_NUC
Gappp 10.0 , Gapext 1.0
Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 457068
Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/podata/1/ina/5B_COMB_seq: *
3: /cgn2_6/podata/1/ina/6A_COMB_seq: *
4: /cgn2_6/podata/1/ina/6B_COMB_seq: *
5: /cgn2_6/podata/1/ina/PCITS_COMB_seq: *
6: /cgn2_6/podata/1/ina/backfile1.seq: *

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.8	61.0	20	3	US-09-428-219-82
2	12.4	59.0	17	3	US-09-998-039-62
3	12.4	59.0	20	4	US-09-998-152A-6154
4	12.2	58.1	20	4	US-09-961-159-78
5	12.2	57.1	21	1	US-07-937-609-5
6	12	57.1	21	3	US-09-029-170-5
7	12	57.1	21	4	US-09-443-745-5
8	11.8	56.2	20	3	US-09-702-327-53
9	11.8	56.2	20	3	US-09-017-467B-256
10	11.8	56.2	20	3	US-09-998-099-62/C
11	11.8	56.2	20	4	US-09-900-920-12
12	11.8	56.2	21	4	US-09-557-472-1359
13	11.8	56.2	20	2	US-09-117-932-361
14	11.6	55.2	20	3	US-09-313-932-485
15	11.6	55.2	20	3	US-09-117-467B-337
16	11.6	55.2	20	4	US-09-998-152A-295
17	11.4	54.3	17	1	US-08-152-313-113
18	11.4	54.3	17	1	US-08-059-223-113
19	11.4	54.3	17	1	US-08-579-197-113
20	11.4	54.3	17	4	US-09-174-432B-479
21	11.4	54.3	17	4	US-09-474-432B-859
22	11.4	54.3	17	4	US-09-476-387-479
23	11.4	54.3	17	4	US-09-476-387-479
24	11.4	54.3	17	5	PCT-US94-12947A-113
25	11.4	54.3	18	2	US-08-257-963B-35
26	11.4	54.3	18	3	US-09-841A-35
27	11.4	54.3	18	5	PCT-US95-07201-35

ALIGNMENTS

Qy	2 AGGACCTGCCAGGU 17	Db	3 AGGACCTGCCAGGU 18																								
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Best Local Similarity	68.8%	DB	3;	Matches	11;	Length	20;	Conservative	3;	DB ID	82	Mismatches	2;	Length	20;	Indels	0;	DB ID	82	Gaps	0;	Length	20;				
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Conservative	3;	DB ID	82	Mismatches	2;	Length	20;	Indels	0;	DB ID	82	Gaps	0;	Length	20;												
Mismatches	2;	Length	20;	Indels	0;	DB ID	82	Gaps	0;	Length	20;																
Indels	0;	DB ID	82	Gaps	0;	Length	20;																				
Gaps	0;	Length	20;																								

RESULT 1
US-09-428-219-82
; Sequence 82, Application US/09428219
; Patent No. 6177273
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; INVENTOR: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN-LINKED KINASE EXPRESSION
; FILE REFERENCE: RIS-0101
; CURRENT APPLICATION NUMBER: US/09/428,219
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-428-219-82

RESULT 2
US-08-998-099-62/C
; Sequence 62, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; APPLICANT: STINCHECOMB, DAN T.
; TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 62
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-08-998-099-62

Query Match 59.0%; Score 12.4; DB 3; Length 17;
Best Local Similarity 54.3%; Pred. No. 8.4e+03;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCUGCCAGUGCU 19
Db 15 CCTGCCATGCT 2

RESULT 3
US-19-198-452A-6154/C
; Sequence 6154, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6154
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-6154

Query Match 59.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 64.3%; Pred. No. 8.6e-03;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 8 UGCCAGUGCU 21
Db 15 TGCCTGTGCTT 2

RESULT 4
US-09-861-159-78/C
; Sequence 78, Application US/09861159
; Patent No. 6485974
; GENERAL INFORMATION:
; APPLICANT: Lex M. Covert
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPN2 EXPRESSION
; FILE REFERENCE: RTS-0243
; CURRENT APPLICATION NUMBER: US/09/861,159
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE: OTHER INFORMATION: Antisense Oligonucleotide
; US-09-861-159-78

Query Match 58.1%; Score 12.2; DB 4; Length 20;
Best Local Similarity 58.8%; Pred. No. 1.1e+04;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 UAGGACCUCCAGUGCU 17
Db 20 TAGTAACTGACAGTCT 4

RESULT 5
US-09-861-159-78

Query Match 57.1%; Score 12; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUSCAGAGUC 18
Db 16 CTGCCAGTCCT 5

RESULT 6
US-08-029-170-5/C
; Sequence 5, Application US/08029170
; Patent No. 6169173
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA

US-07-937-609-5/C
; Sequence 5, Application US/07937609
; Patent No. 5319073
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/029,170
 FILING DATE: 19930110
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,609
 FILING DATE: 02-SEP-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/928,033
 FILING DATE: 11-AUG-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/861,769
 FILING DATE: 01-APR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/831,248
 FILING DATE: 07-FEB-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/928,033
 FILING DATE: 11-AUG-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/861,769
 FILING DATE: 01-APR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/928,033
 FILING DATE: 07-FEB-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 40399/166 NIHD
 TELEPHONE: (703)856-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 PRIORITY SEQUENCE FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPLOGY: linear
 -029-170-5
 T 7
 Query Match 57.1%; Score 12; DB 3; Length 21;
 Best Local Similarity 75.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;
 Matches 9; Conservative 3; Mismatches 0; ;
 Sequence 877, Application US/09443745
 Patent No. 672063
 GENERAL INFORMATION:
 APPLICANT: WANK, Stephen A.
 TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
 TITLE OF INVENTION: CHORBYCYSTOKININ RECEPTOR-ENCODING DNA
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/443,745
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,609
 FILING DATE: 02-SEP-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/928,033
 FILING DATE: 11-AUG-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/861,769
 FILING DATE: 01-APR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/831,248
 FILING DATE: 07-FEB-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 40399/166 NIHD
 TELEPHONE: (703)856-9300
 TELEFAX: 899149
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPLOGY: linear
 US-09-443-745-5
 T 7
 Query Match 57.1%; Score 12; DB 4; Length 21;
 Best Local Similarity 75.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;
 Matches 9; Conservative 3; Mismatches 0; ;
 Sequence 877, Application US/09657472
 Patent No. 672063
 GENERAL INFORMATION:
 APPLICANT: Lander, Eric S.
 APPLICANT: Cargill, Michele
 APPLICANT: Ireland, James S.
 APPLICANT: Boik, Stacey
 APPLICANT: Daley, George O.
 APPLICANT: McCarthy, Jeanette J.
 TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
 FILE REFERENCE: 2825.107-001
 CURRENT APPLICATION NUMBER: US/09/657,472
 CURRENT FILING DATE: 2000-09-07
 PRIORITY APPLICATION NUMBER: US 60/153,357
 PRIORITY FILING DATE: 1999-09-10
 PRIORITY APPLICATION NUMBER: US 60/220,947
 PRIORITY FILING DATE: 2000-07-26
 PRIORITY APPLICATION NUMBER: US 60/225,724
 PRIORITY FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 2551
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 877
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-657-472-877
 Query Match 57.1%; Score 12; DB 4; Length 21;
 Best Local Similarity 64.3%; Pred. No. 1.4e+04;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CCUGCCAGUCUCU 19

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Db' 1 CCTGGCAGTCGCT 14
; CURRENT APPLICATION NUMBER: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-702-327-53

Query Match 56.2%; Score 11.8; DB 3; Length 20;
Best Local Similarity 73.3%; Pred. No. 1.7e+04; 1; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 2; Prior Application Number: US/09/702,327
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-702-327-53

RESULT 10
US-09-517-467B-256/c
; Sequence 256, Application US/09517467B
; Patent No. 6451602
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION
; CURRENT APPLICATION NUMBER: US/09/517,467B
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/517,467
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 345
; SEQ ID NO 256
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-517-467B-256

Query Match 56.2%; Score 11.8; DB 3; Length 20;
Best Local Similarity 73.3%; Pred. No. 1.7e+04; 2; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 2; Prior Application Number: US/09/517,467
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 345
; SEQ ID NO 256
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-517-467B-256

RESULT 11
US-09-657-346A-69
; Sequence 69, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CALRETICULIN EXPRESSION
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0135
; CURRENT APPLICATION NUMBER: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-657-346A-69

Query Match 56.2%; Score 11.8; DB 4; Length 20;
Best Local Similarity 73.3%; Pred. No. 1.7e+04; 2; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 2; Prior Application Number: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-657-346A-69

RESULT 12
US-09-900-920-12/c
; Sequence 12, Application US/09900920
; Patent No. 6696562
; GENERAL INFORMATION:
; APPLICANT: Schnitz-Cherry, Stacey
; APPLICANT: Kelley, Laura
; APPLICANT: Koci, Matthew
; APPLICANT: Seal, Bruce
; TITLE OF INVENTION: No. 6696562 Avian Astrovirus
; FILE REFERENCE: turkeyastrovirus
; CURRENT APPLICATION NUMBER: US/09/900,920
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,312
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Turkey Astrovirus
; US-09-900-920-12

Query Match 56.2%; Score 11.8; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.7e+04; 3; Mismatches 2; Indels 0; Gaps 0;
Matches 10; Conservative 3; Prior Application Number: US/09/900,920
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Turkey Astrovirus
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-900-920-12

RESULT 13
US-09-657-472-1359/c
; Sequence 1359, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Boik, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; CURRENT FILING DATE: 2000-09-07
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16

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; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1359
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-657-472-1359

RESULT 14
US-08-117-952-361/C
; Sequence 361, Application US/08117952
; Patent No. 5551760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 361:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-361

Query Match 55.2%; Score 11.6; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 2.1e+04; Matches 10; Conservative 4; Mismatches 4; Qy. 4 GACGCCAGCAGUCUCCT 21 Db 18 GGCCCTGGCAGGATATT 1

RESULT 15
US-03-313-932-485/C
; Sequence 485, Application US/03313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shahanan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-  

; FILE REFERENCE: ISPR-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 485
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetic
; US-09-313-932-485

Query Match 55.2%; Score 11.6; DB 3; Length 20;
Best Local Similarity 61.1%; Pred. No. 2.1e+04; Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy. 1 UAGGACCCUGCCAGUCUC 18 Db 18 TAGGAGCTCCCTGGCTC 1

Search completed: September 17, 2005, 09:08:20
Job time : 96 SECs

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 Qy ||||||| ||||||| ||||||| |||||
 Db 1 UAGGACCUCCAGUGUCUTT 21

RESULT 2
 US-10-424-041-41/C
 ; Sequence 41, Application US/10424041
 ; Publication No. US20040215006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Thomas Condon
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
 ; CURRENT APPLICATION NUMBER: US/10/424, 041
 ; CURRENT FILING DATE: 2003-04-25
 ; NUMBER OF SEQ ID NOS: 184
 ; SEQ ID NO: 41
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 ; US-10-424-041-41

Query Match 85.7%; Score 18; DB 20; Length 20;
 Best Local Similarity 77.8%; Pred. No. 33;
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 UAGGACCUCCAGUGUC 18
 Db 18 TAGGACCTGCCAGTC 1

RESULT 3
 US-10-424-041-132
 ; Sequence 132, Application US/10424041
 ; Publication No. US20040215006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Thomas Condon
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
 ; CURRENT APPLICATION NUMBER: US/10/424, 041
 ; CURRENT FILING DATE: 2003-04-25
 ; NUMBER OF SEQ ID NOS: 184
 ; SEQ ID NO: 132
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; US-10-424-041-132

Query Match 85.7%; Score 18; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 UAGGACCUCCAGUGUC 18
 Db 3 UAGGACCUCCAGUGUC 20

RESULT 4
 US-10-424-041-56/C
 ; Sequence 56, Application US/10424041
 ; Publication No. US20040215006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Thomas Condon
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
 ; CURRENT APPLICATION NUMBER: US/10/424, 041
 ; CURRENT FILING DATE: 2003-04-25
 ; NUMBER OF SEQ ID NOS: 184
 ; SEQ ID NO: 41
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 ; US-10-424-041-56

Query Match 81.0%; Score 17; DB 20; Length 20;
 Best Local Similarity 76.5%; Pred. No. 1.1e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 UAGGACCUCCAGUGCU 17
 Db 17 TAGGACCTGCCAGTC 1

RESULT 5
 US-10-424-041-144
 ; Sequence 144, Application US/10424041
 ; Publication No. US20040215006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Thomas Condon
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
 ; CURRENT APPLICATION NUMBER: US/10/424, 041
 ; CURRENT FILING DATE: 2003-04-25
 ; NUMBER OF SEQ ID NOS: 184
 ; SEQ ID NO: 144
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: M. musculus
 ; FEATURE:
 ; US-10-424-041-144

Query Match 81.0%; Score 17; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 UAGGACCUCCAGUGCU 17
 Db 4 UAGGACCUCCAGUGCU 20

RESULT 6
 US-10-304-082-11
 ; Sequence 11, Application US/10304082
 ; Publication No. US20040102401A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
 ; CURRENT APPLICATION NUMBER: US/10/304, 082
 ; CURRENT FILING DATE: 2002-11-22
 ; NUMBER OF SEQ ID NOS: 78
 ; SEQ ID NO: 11
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide

RESULT 7
US-10-304-082-48/c
; Sequence 48 Application US/10304082
; Publication No. US20040102401A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: PTS-0037
; CURRENT APPLICATION NUMBER: US/10/304,082
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; US-10-304-082-48

Query Match 64.8%; Score 13.6; DB 19; Length 20;
Best Local Similarity 70.0%; Pred. No. 5.9e+03;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCTUGGCCAGGUCCUTT 21
Db 1 AGGCACTGCCAGGGCTATT 20

RESULT 8
US-10-847-918-2129
; Sequence 2129, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slomim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-020000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2129
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
; US-10-847-918-2129

Query Match 64.8%; Score 13.6; DB 21; Length 21;
Best Local Similarity 75.0%; Pred. No. 6e+03; Mismatches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UAGGACCTUGGCCAGGUCCUTT 20
Db 2 UCGGAGCUGCCAGGUCCUTT 21

RESULT 9
US-10-924-375-91/c
; Sequence 91 Application US/10024375
; Publication No. US20050130190A1
; GENERAL INFORMATION:
; APPLICANT: Antzalevitch, Charles
; APPLICANT: Brngada, Ramon
; APPLICANT: Hong, Kui
; TITLE OF INVENTION: Mutations in Ion Channel Proteins Associated With Sudden Cardiac FILE REFERENCE: 1395-2
; CURRENT APPLICATION NUMBER: US/10/924,375
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: 60/197,256
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
; US-10-924-375-91

Query Match 63.8%; Score 13.4; DB 22; Length 18;
Best Local Similarity 66.7%; Pred. No. 7.5e+03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACCUGGAGGUCCUT 19
Db 16 ACCUGGAGGUCCUT 2

RESULT 10
US-11-039-629-89
; Sequence 89 Application US/11039629
; Publication No. US20050164271A1
; GENERAL INFORMATION:
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Freier, Susan M.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: MODULATION OF GLUCOCORTICOID RECEPTOR
; TITLE OF INVENTION: MODULATION OF GLUCOCORTICOID RECEPTOR
; FILE REFERENCE: PTS-053205
; CURRENT APPLICATION NUMBER: US/11/039,629
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/538,173
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/550,191
; CURRENT APPLICATION NUMBER: US/11/039,629
; CURRENT FILING DATE: 2005-01-20
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSBQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Antisense Compound
; OTHER INFORMATION: Antisense Compound
; US-11-039-629-89

Query Match 62.9%; Score 13.2; DB 24; Length 20;
Best Local Similarity 61.1%; Pred. No. 9.5e+03;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GACCTUGGCCAGGUCCUT 21
Db 3 GTCCCTCCACTGCCTT 20

RESULT 11

US*10-156-306-5959
; Sequence 59, Application US/10156306
; Publication No. US20030115017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH301-664-A
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 803
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5959
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306-5959

Query Match 61.0%; Score 12.8; DB 15; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.5e+04; 0; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAGGACCCGAGUC 16
Db 1 UAGGGCCGGCCAGUC 16

RESULT 12
US-10-156-306-7065
; sequence 7065, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH301-664-A (400/150)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 803
; SOFTWARE: PatentIn version 3.0
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306-7065

Query Match 61.0%; Score 12.8; DB 15; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.5e+04; 0; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAGGACCCGAGUC 16
Db 2 UAGGGCCGGCCAGUC 17

RESULT 13
US-10-282-174-310/C
; Sequence 310, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelobi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10

Query Match 61.0%; Score 12.8; DB 17; Length 20;
Best Local Similarity 68.8%; Pred. No. 1.5e+04; 0; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGACCCGAGUCU 17
Db 3 AGGACCTTCAGTCT 18

RESULT 15
US-10-671-395-720/C
; Sequence 720, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K.

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 11791-US
CURRENT APPLICATION NUMBER: US10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
SEQ ID NO: 720
LENGTH: 20
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: Human PGE2 antisense
S-10-671-395-720

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GenCore version 5.1.6

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112: /cgn2_6/ptodata/1/pna/US6042_COMB.seq: *
113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq: *
114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq: *
115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq: *
116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score	Match	Length	DB	ID	Description	OTHER INFORMATION: Description of Artificial Sequence: Synthetic Oligonucleotide
1	21	100.0	21	62	US-10-738-413-1	; OTHER INFORMATION: oligonucleotide
2	18	85.7	20	54	US-10-424-041-41	Query Match
3	18	85.7	20	54	US-10-424-041-132	Best Local Similarity 100.0%; Score 21; DB 62; Length 21; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4	17	81.0	20	54	US-10-424-041-56	Sequence 145, APP
5	17	81.0	20	54	US-10-424-041-144	Sequence 56, APP
6	14.8	70.5	19	60	US-10-714-333A-239150	Sequence 239150, APP
7	14.2	67.6	19	60	US-10-714-333A-62335	Sequence 62335, A
8	14.2	67.6	19	60	US-10-714-333A-1045669	Sequence 1045669, APP
9	14.2	67.6	19	60	US-10-714-333A-1495857	Sequence 1495857, APP
10	13.8	65.7	19	60	US-10-714-333A-113284	Sequence 113284, APP
11	13.8	65.7	19	60	US-10-714-333A-113286	Sequence 113286, APP
12	13.8	65.7	21	62	US-10-770-726-7139	RESULT 2
13	13.6	64.8	20	52	PCT-US03-37756-49	US-10-424-041-41/C
14	13.6	64.8	20	52	US-10-304-082-11	; Sequence 41, Application US/10424041
15	13.6	64.8	20	52	US-10-304-082-48	; GENERAL INFORMATION:
16	13.6	64.8	21	63	PCT-US04-15645-2129	APPLICANT: C. Frank Bennett
17	13.6	64.8	18	65	US-10-847-918-2129	APPLICANT: Thomas Condon
18	13.6	64.8	18	65	US-10-224-375-91	APPLICANT: Susan M. Freier
19	13.4	63.8	19	60	US-10-714-333A-329055	APPLICANT: Kenneth W. Dobbie
20	13.4	63.8	19	60	US-10-714-333A-329070	TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
21	13.4	63.8	19	60	US-10-714-333A-329075	FILE REFERENCE: B101-005US
22	13.4	63.8	19	60	US-10-714-333A-1057362	CURRENT APPLICATION NUMBER: US/10/424,041
23	13.4	63.8	19	60	US-10-714-333A-150015	CURRENT FILING DATE: 2003-04-25
24	13.4	63.8	19	60	US-10-714-333A-150013	NUMBER OF SEQ ID NOS: 184
25	13.4	63.8	19	60	US-10-714-333A-35790	SEQ ID NO 41
26	13.2	62.9	19	60	US-10-714-333A-36093	LENGTH: 20
27	13.2	62.9	19	60	US-10-714-333A-36186	TYPE: DNA
28	13.2	62.9	19	60	US-10-714-333A-59186	ORGANISM: Artificial Sequence
29	13.2	62.9	19	60	US-10-714-333A-15298	FEATURE: OTHER INFORMATION: Antisense Oligonucleotide
30	13.2	62.9	19	60	US-10-714-333A-115378	SEQUENCE: US-10-424-041-41
31	13.2	62.9	19	60	US-10-714-333A-115378	Query Match
32	13.2	62.9	19	60	US-10-714-333A-115577	Best Local Similarity 85.7%; Score 18; DB 54; Length 20; Matches 14; Conservative 7.7%; Pred. No. 3e-02; Mismatches 0; Indels 0; Gaps 0;
33	13.2	62.9	19	60	US-10-714-333A-612131	Sequence 612131, APP
34	13.2	62.9	19	60	US-10-714-333A-612153	Sequence 612153, APP
35	13.2	62.9	19	60	US-10-714-333A-1207022	Sequence 1207022, APP
36	13.2	62.9	19	60	US-10-714-333A-1342729	Sequence 1342729, APP
37	13.2	62.9	19	60	US-10-714-333A-1495844	Sequence 1495844, APP
38	13.2	62.9	20	90	US-60-216-745-9885	Sequence 9885, APP
39	13.2	62.9	21	62	US-10-770-726-36005	Sequence 36005, APP
40	13.2	62.9	21	62	US-10-770-726-36006	Sequence 36006, APP
41	13.2	62.9	21	62	PCT-US02-25943-16735	Sequence 16735, APP
42	13.1	61.9	15	50	PCT-US02-25943-16736	Sequence 16736, APP
43	13.1	61.9	15	50	US-10-227-565-16735	Sequence 16735, APP
44	13.1	61.9	15	50	US-10-227-565-16735	Sequence 16735, APP
45	13.1	61.9	15	53	US-10-367-832A-16735	Sequence 16735, APP

ALIGNMENTS

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; FILE REFERENCE: BILO0005US
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 132
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE: 
; US-10-424-041-132

Query Match 85.7%; Score 18; DB 54; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 UAGGACCCUGGAGUGUC 18
Db 3 UGGACCUGCCAGUGUC 20

RESULT 4
US-10-424-041-56/c
; Sequence 56, Application US/10424041
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BILO0005US
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: 
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-424-041-56

Query Match 81.0%; Score 17; DB 54; Length 20;
Best Local Similarity 76.5%; Pred. No. 9.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 UAGGACCCUGGAGUGUC 17
Db 17 TGGACCTGCCAGCT 1

RESULT 5
US-10-424-041-144
; Sequence 144, Application US/10424041
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BILO0005US
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 144
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE: 
; US-10-424-041-144

Query Match 81.0%; Score 17; DB 54; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 UAGGACCCUGGAGUGUC 17
Db 3 UGGACCUGCCAGUGUC 20

RESULT 6
US-10-714-333A-239150
; Sequence 239150, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmaccon, Inc.
; APPLICANT: Khorrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 1591911
; SEQ ID NO 239150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-714-333A-239150

Query Match 70.5%; Score 14.8; DB 60; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.2e+04; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GACCUGCCAGUGUCUTT 21
Db 2 GACCUGCCAGUGUCU 19

RESULT 7
US-10-714-333A-62335
; Sequence 62335, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmaccon, Inc.
; APPLICANT: Khorrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarling, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 1591911
; SEQ ID NO 62335
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-714-333A-62335

Query Match 67.6%; Score 14.2; DB 60; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+04; Mismatches 3; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGACCUCCAGUGUCUTT 21
Db 3 ||||| ||||| :::

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RESULT 8 US-10-714-333A-1045669
; Sequence 1045669, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khrorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1045669
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1045669

Query Match Score 14.2; DB 60; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+04;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGACCCGCGAGGUCUCC 21
Db 1 GGACCCGCGAGGUCUCC 19

RESULT 9 US-10-714-333A-1492857
; Sequence 1492857, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khrorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1045669
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1045669

Query Match Score 14.2; DB 60; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+04;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGACCCGCGAGGUCUCC 21
Db 1 GGACCCGCGAGGUCUCC 19

RESULT 10 US-10-714-333A-113284
; Sequence 113284, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khrorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 113284
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-113284

Query Match Score 13.8; DB 60; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.8e+04;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 5 ACCUCCGAGGUCUCC 21
Db 2 ACCUCCGAGGUCUCC 18

RESULT 11 US-10-714-333A-113286
; Sequence 113286, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khrorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 113286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-113286

Query Match Score 13.8; DB 60; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.8e+04;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 5 ACCUCCGAGGUCUCC 21
Db 3 ACCUCCGAGGUCUCC 19

RESULT 12 US-10-714-333A-113286
; Sequence 113286, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khrorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 113286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-113286

Query Match Score 13.8; DB 60; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.8e+04;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 5 ACCUCCGAGGUCUCC 21
Db 3 ACCUCCGAGGUCUCC 19

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GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; SEQ ID NO: 7139
; US-10-770-726-7139

Query Match 65.7%; Score 13.8; DB 62; Length 21;
Best Local Similarity 70.6%; Pred. No. 3.9e+04; 2; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 2;

Qy 2 AGGACUGGCCAGUGUC 18
Db 17 AGGACCTGCCGTCGTC 1

RESULT 13
PCT-US03-37756-12
; Sequence 12, Application PC/TUS0337756
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: ISPT-1008
; CURRENT APPLICATION NUMBER: PCT/US03/37756
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO: 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Modulation of Jagged 1 expression
; US-10-304-082-11

Query Match 64.8%; Score 13.6; DB 2; Length 20;
Best Local Similarity 70.0%; Pred. No. 4.9e+04; 4; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 4;

Qy 2 AGGACUGGCCAGUGUC 21
Db 1 AGGACCTGCCGTCGTC 20

RESULT 14
PCT-US03-37756-49/C
; Sequence 49, Application PC/TUS0337756
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: ISPT-1008
; CURRENT APPLICATION NUMBER: PCT/US03/37756
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,082
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence
; PCT-US03-37756-12

Query Match 64.8%; Score 13.6; DB 2; Length 20;
Best Local Similarity 70.0%; Pred. No. 4.9e+04; 4; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 4;

Qy 2 AGGACUGGCCAGUGUC 21
Db 1 AGGACCTGCCGTCGTC 20

Search completed: September 17, 2005, 09:49:56
Job time : 2489 sec

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ON nucleic - nucleic search, using sw model
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25: /cgpn2_6/ptodata/1/pna/US11_NEW_COMB_seq6: *
26: /cgpn2_6/ptodata/1/pna/US60_NEW_COMB_seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	2	PCT-US04-39941-1 Sequence 1, Appl Sequence 41, Appl Sequence 132, App Sequence 344173, Sequence 682886, Sequence 21, Conserva Sequence 56, Appl
2	18	85.7	20	21	US-11-071-788-41 Sequence 132, App Sequence 344173, Sequence 682886, Sequence 56, Appl
3	19	85.7	20	21	US-11-071-788-132 Sequence 132, App Sequence 344173, Sequence 682886, Sequence 56, Appl
4	17.8	84.8	21	12	US-10-605-923-344173 Sequence 132, App Sequence 344173, Sequence 682886, Sequence 56, Appl
5	17.8	84.8	21	12	US-10-605-924-682886 Sequence 132, App Sequence 344173, Sequence 682886, Sequence 56, Appl
6	17	84.8	21	16	US-10-310-914-964352 Sequence 132, App Sequence 344173, Sequence 682886, Sequence 56, Appl
7	81.0	20	21	21	US-11-071-788-144 Sequence 132, App Sequence 344173, Sequence 682886, Sequence 56, Appl

RESULT 1
PCT-US04-39941-1
; Sequence 1, Application PC/TUS04/39941
; GENERAL INFORMATION:
; APPLICANT: AVON PRODUCTS, INC.
; TITLE OF INVENTION: SI-RNA-MEDIATED GENE SILENCING TECHNOLOGY TO INHIBIT
; TITLE OF INVENTION: TYROSINASE AND REDUCE PIGMENTATION
; TITLE REFERENCE: SC6U-WO
; CURRENT APPLICATION NUMBER: PCT/US04/39941
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: 10/738,413
; PRIOR FILING DATE: 2003-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic
; FEATURE: OTHER INFORMATION: Description of Oligonucleotide
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
; OTHER INFORMATION: Other Information: PCT-US04-39941-1
Query Match 100.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 US-11-071-788-41/C
 ; Sequence 41, Application US/11071788
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Thomas Condon
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: James Karras
 ; APPLICANT: Susan Fitch
 ; APPLICANT: Ravi Jain
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
 ; FILE REFERENCE: BNDL-001785.P1
 ; CURRENT APPLICATION NUMBER: US/11/071,788
 ; CURRENT FILING DATE: 2005-03-02
 ; PRIOR APPLICATION NUMBER: US 10/424,041
 ; PRIOR FILING DATE: 2003-04-25
 ; PRIOR APPLICATION NUMBER: US 10/704,263
 ; PRIOR FILING DATE: 2003-11-06
 ; PRIOR APPLICATION NUMBER: US 10/889,101
 ; PRIOR FILING DATE: 2004-07-12
 ; PRIOR APPLICATION NUMBER: US 60/486,652
 ; PRIOR FILING DATE: 2003-07-12
 ; PRIOR APPLICATION NUMBER: US 10/889,447
 ; PRIOR FILING DATE: 2004-07-12
 ; PRIOR APPLICATION NUMBER: US 60/486,670
 ; PRIOR FILING DATE: 2003-07-12
 ; PRIOR APPLICATION NUMBER: US 10/498,704
 ; PRIOR FILING DATE: 2004-06-14
 ; PRIOR APPLICATION NUMBER: PCT/US02/39873
 ; PRIOR FILING DATE: 2002-12-13
 ; PRIOR APPLICATION NUMBER: US 10/029,517
 ; PRIOR FILING DATE: 2001-12-20
 ; SEQ ID NO: 41
 ; LENGTH: 20
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 ; US-11-071-788-41

Query Match
 Best Local Similarity 77.8%; Score 18; DB 21; Length 20;
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGGACCCUGCCAGUCUC 18
 Db 18 TAGGACCTGCCAGTCCTC 1

RESULT 3
 US-11-071-788-13/2
 ; Sequence 13, Application US/11071788
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Thomas Condon
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: James Karras
 ; APPLICANT: Susan Fitch
 ; APPLICANT: Ravi Jain
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
 ; FILE REFERENCE: BNDL-001785.P1
 ; CURRENT APPLICATION NUMBER: US/11/071,788
 ; CURRENT FILING DATE: 2005-03-02
 ; PRIOR APPLICATION NUMBER: US 10/424,041
 ; PRIOR FILING DATE: 2003-04-25

Query Match
 Best Local Similarity 85.7%; Score 18; DB 21; Length 20;
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGGACCCUGCCAGUCUC 18
 Db 3 UAGGACCCUGCCAGUCUC 20

RESULT 4
 US-10-605-923-344173
 ; Sequence 344173, Application US/10605923
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSETTA GENOMICS LTD
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
 ; FILE REFERENCE: 55000
 ; CURRENT APPLICATION NUMBER: US/10/605,923
 ; CURRENT FILING DATE: 2003-11-06
 ; NUMBER OF SEQ ID NOS: 1515668
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 344173
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; US-10-605-923-344173

Query Match
 Best Local Similarity 84.8%; Score 17.8; DB 12; Length 21;
 Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAGGACCCUGCCAGUCUC 21
 Db 1 TGGGACCTGCCAGTCCTG 21

RESULT 5
 US-10-605-924-682886/C
 ; Sequence 682886, Application US/10605924
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSETTA GENOMICS LTD
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
 ; TITLE OF INVENTION: US8S THEREOF
 ; FILE REFERENCE: 55004
 ; CURRENT APPLICATION NUMBER: US/10/605,924
 ; CURRENT FILING DATE: 2003-11-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 682886

RESULT 6
 Query Match 84.8%; Score 17.8; DB 12; Length 21;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 UAGGACCCUGCCAGUGUCU 21
 :|||||:|||||:|||:
 Db 21 TGGGACCTGCCAGTCCTGT 1

RESULT 6
 Query Match 84.8%; Score 17.8; DB 12; Length 21;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 UAGGACCCUGCCAGUGUCU 21
 :|||||:|||||:|||:
 Db 21 TGGGACCTGCCAGTCCTGT 1

GENERAL INFORMATION:
 Sequence 682886, Application US/10310914A
 APPLICANT: Bentwich, Isaac
 APPLICANT: Shiler, Kuznet
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 FILE REFERENCE: 06087-0200.CPUS01
 CURRENT APPLICATION NUMBER: US10/310,914A
 CURRENT FILING DATE: 2002-12-06
 NUMBER OF SEQ ID NOS: 1388402
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 682886
 LENGTH: 21
 TYPE: RNA
 ORGANISM: Human
 US-10-310-914A-682886

Query Match 84.8%; Score 17.8; DB 16; Length 21;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 UAGGACCCUGCCAGUGUCU 21
 :|||||:|||||:|||:
 Db 21 TGGGACCTGCCAGTCCTGT 1

RESULT 7
 US-11-071-788-56/c
 Sequence 56, Application US/11071788
 GENERAL INFORMATION:
 APPLICANT: C. Frank Bennett
 APPLICANT: Thomas Condon
 APPLICANT: Susan M. Freier
 APPLICANT: James Karras
 APPLICANT: Susan Fitch
 APPLICANT: Ravi Jain
 APPLICANT: Kenneth W. Dobie
 TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
 FILE REFERENCE: BNDL-0017US.P1
 CURRENT APPLICATION NUMBER: US/11/071,788
 PRIOR APPLICATION NUMBER: US 10/424,041
 PRIOR FILING DATE: 2003-04-25
 PRIOR APPLICATION NUMBER: US 10/704,263
 PRIOR FILING DATE: 2003-11-05
 PRIOR APPLICATION NUMBER: US 10/889,101
 PRIOR FILING DATE: 2004-07-12
 PRIOR APPLICATION NUMBER: US 60/485,652
 PRIOR FILING DATE: 2003-07-12
 PRIOR APPLICATION NUMBER: US 10/889,447
 PRIOR FILING DATE: 2000-07-12
 PRIOR APPLICATION NUMBER: US 60/486,670
 PRIOR FILING DATE: 2003-07-12
 PRIOR APPLICATION NUMBER: US 60/498,704
 PRIOR FILING DATE: 2004-06-14
 PRIOR APPLICATION NUMBER: PCT/US02/39873
 PRIOR FILING DATE: 2002-12-13
 PRIOR APPLICATION NUMBER: US 10/029,517
 PRIOR FILING DATE: 2001-12-20
 NUMBER OF SEQ ID NOS: 184
 SEQ ID NO 144
 LENGTH: 20
 TYPE: DNA
 ORGANISM: M. musculus
 FEATURE:
 US-11-071-788-144

Query Match 81.0%; Score 17; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UAGGACCCUGCCAGUGUCU 17
 :|||||:|||||:|||:
 Db 4 UAGGACCCUGCCAGUGUCU 20

RESULT 9
 Query Match 81.0%; Score 17; DB 21; Length 20;
 Best Local Similarity 76.5%; Pred. No. 3.6e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UAGGACCCUGCCAGUGUCU 17
 :|||||:|||||:|||:
 Db 17 TAGGACCCUGCCAGUGUCU 1

GENERAL INFORMATION:
 Sequence 144, Application US/11071788
 GENERAL INFORMATION:
 APPLICANT: C. Frank Bennett
 APPLICANT: Thomas Condon
 APPLICANT: Susan M. Freier
 APPLICANT: James Karras
 APPLICANT: Susan Fitch
 APPLICANT: Ravi Jain
 APPLICANT: Kenneth W. Dobie
 TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
 FILE REFERENCE: BNDL-0017US.P1
 CURRENT APPLICATION NUMBER: US/11/071,788
 PRIOR APPLICATION NUMBER: US 10/424,041
 PRIOR FILING DATE: 2003-04-25
 PRIOR APPLICATION NUMBER: US 10/704,263
 PRIOR FILING DATE: 2003-11-05
 PRIOR APPLICATION NUMBER: US 10/889,101
 PRIOR FILING DATE: 2004-07-12
 PRIOR APPLICATION NUMBER: US 60/485,652
 PRIOR FILING DATE: 2003-07-12
 PRIOR APPLICATION NUMBER: US 10/889,447
 PRIOR FILING DATE: 2000-07-12
 PRIOR APPLICATION NUMBER: US 60/486,670
 PRIOR FILING DATE: 2003-07-12
 PRIOR APPLICATION NUMBER: US 60/498,704
 PRIOR FILING DATE: 2004-06-14
 PRIOR APPLICATION NUMBER: PCT/US02/39873
 PRIOR FILING DATE: 2002-12-13
 PRIOR APPLICATION NUMBER: US 10/029,517
 PRIOR FILING DATE: 2001-12-20
 NUMBER OF SEQ ID NOS: 184
 SEQ ID NO 144
 LENGTH: 20
 TYPE: DNA
 ORGANISM: M. musculus
 FEATURE:
 US-11-071-788-144

Query Match 81.0%; Score 17; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UAGGACCCUGCCAGUGUCU 17
 :|||||:|||||:|||:
 Db 4 UAGGACCCUGCCAGUGUCU 20

RESULT 9
 Query Match 81.0%; Score 17; DB 21; Length 20;
 Best Local Similarity 76.5%; Pred. No. 3.6e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UAGGACCCUGCCAGUGUCU 17
 :|||||:|||||:|||:
 Db 17 TAGGACCCUGCCAGUGUCU 1

GENERAL INFORMATION:
 Sequence 21186, Application US/10604985A
 NUMBER OF SEQ ID NOS: 184
 SEQ ID NO 56
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide
 US-11-071-788-56

GENERAL INFORMATION:
 APPLICANT: ROSETTA GENOMICS LTD
 TITLE OF INVENTION: BIOMINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
 FILE REFERENCE: 55011
 CURRENT APPLICATION NUMBER: US/10/604, 985A
 CURRENT FILING DATE: 2003-08-29
 NUMBER OF SEQ ID NOS: 97967
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 21186
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Human
 US-10-604-985A-21186

Query Match 78.1%; Score 16.4; DB 11; Length 21;
 Best Local Similarity 72.2%; Pred. No. 7.3e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 13; Conservative 4; SEQ ID NO: 21186
 QY 1 UAGGACCCUGCCAGUGUC 18
 Db 4 TGGGACCTGCGCAGTC 21

RESULT 10
 US-10-604-985-21186
 CURRENT APPLICATION NUMBER: US/10/604, 985
 Sequence 21186, Application US/10/604, 985
 GENERAL INFORMATION:
 APPLICANT: ROSETTA GENOMICS LTD
 TITLE OF INVENTION: BIOMINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
 FILE REFERENCE: 55011
 CURRENT APPLICATION NUMBER: US/10/604, 985
 NUMBER OF SEQ ID NOS: 97947
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 21186
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-604-985-21186

Query Match 78.1%; Score 16.4; DB 12; Length 21;
 Best Local Similarity 72.2%; Pred. No. 7.3e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 13; Conservative 4; Mismatches 1; SEQ ID NO: 21186
 QY 1 UAGGACCCUGCCAGUGUC 18
 Db 4 TGGGACCTGCGCAGTC 21

RESULT 11
 US-10-605-923-784389/C
 Sequence 784389, Application US/10/605, 923
 GENERAL INFORMATION:
 APPLICANT: ROSETTA GENOMICS LTD
 TITLE OF INVENTION: BIOMINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
 FILE REFERENCE: 55000
 CURRENT APPLICATION NUMBER: US/10/605, 923
 CURRENT FILING DATE: 2003-11-06
 NUMBER OF SEQ ID NOS: 1515668
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 784389
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Homo Sapiens
 US-10-605-923-784389

Query Match 72.4%; Score 15.2; DB 12; Length 21;
 Best Local Similarity 60.0%; Pred. No. 2.9e+03; Mismatches 5; Indels 0; Gaps 0;
 Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

RESULT 12
 US-10-605-924-964352
 Sequence 964352, Application US/10/605, 924
 CURRENT APPLICATION NUMBER: US/10/605, 924
 Sequence 964352, Application US/10/605, 924
 GENERAL INFORMATION:
 APPLICANT: ROSETTA GENOMICS LTD
 TITLE OF INVENTION: BIOMINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
 FILE REFERENCE: 55004
 CURRENT APPLICATION NUMBER: US/10/605, 924
 NUMBER OF SEQ ID NOS: 1388402
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 964352
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Homo Sapiens
 US-10-605-924-964352

Query Match 72.4%; Score 15.2; DB 13; Length 21;
 Best Local Similarity 60.0%; Pred. No. 2.9e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

RESULT 13
 US-10-310-914A-964352
 Sequence 964352, Application US/10/310, 914A
 CURRENT APPLICATION NUMBER: US/10/310, 914A
 Sequence 964352, Application US/10/310, 914A
 GENERAL INFORMATION:
 APPLICANT: Bentwich, Isaac
 APPLICANT: Shiller, Kvusat
 APPLICANT: Bentwich, Isaac
 TITLE OF INVENTION: Biominformatically detectable group of novel regulatory genes and
 FILE REFERENCE: 6087, 0200, CPS01
 CURRENT APPLICATION NUMBER: US/10/310, 914A
 CURRENT FILING DATE: 2002-12-06
 NUMBER OF SEQ ID NOS: 1388402
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 964352
 LENGTH: 21
 TYPE: RNA
 ORGANISM: Human
 US-10-310-914A-964352

Query Match 72.4%; Score 15.2; DB 16; Length 21;
 Best Local Similarity 80.0%; Pred. No. 2.9e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

RESULT 14
 PCT-US03-36797-239150
 Sequence 239150, Application PCT/US03/36797
 CURRENT APPLICATION NUMBER: US/10/605, 924
 Sequence 239150, Application PCT/US03/36797
 GENERAL INFORMATION:
 APPLICANT: Dharmam, Inc.
 APPLICANT: Kivorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Read, Steven
 APPLICANT: Searling, Stephen
 TITLE OF INVENTION: Methods and Compositions for Improving
 TITLE OF INVENTION: siRNA Functionality

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FILE REFERENCE: 13499PCT
CURRENT APPLICATION NUMBER: PCT/US03/36787
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502, 050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426, 137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 239150
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
PCT-US03-36787-239150

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Query Match 70.5%; Score 14.8; DB 2; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.6e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 GACCUGGCCAGUGCUCU TT 21
Db 2 GACCUGGCCAGUGCUCU UU 19

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RESULT 15
US-10-714-333B-239150
; Sequence 239150, Application US/10714333B
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khorrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarlinge, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10714,333B
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 239150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333B-239150

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Query Match 70.5%; Score 14.8; DB 14; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.6e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 GACCUGGCCAGUGCUCU TT 21
Db 2 GACCUGGCCAGUGCUCU UU 19

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Search completed: September 17, 2005, 10:11:06
Job time : 1264 sec

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